

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Fisher, Douglas A.
Gooding, Douglas H.
Streeter, David Gray
- (ii) TITLE OF THE INVENTION: CYCLIC-GMP PHOSPHODIESTERASE
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Dr.
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Filed Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0442 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650-855-0555
 - (B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 593 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: PROSNOT06
 - (B) CLONE: 828228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Gly	Ser	Gly	Ser	Ser	Ser	Tyr	Arg	Pro	Lys	Ala	Ile	Tyr	Leu	Asp
1				5					10					15	
Ile	Asp	Gly	Arg	Ile	Gln	Lys	Val	Ile	Phe	Ser	Lys	Tyr	Cys	Asn	Ser
			20					25					30		
Ser	Asp	Ile	Met	Asp	Leu	Phe	Cys	Ile	Ala	Thr	Gly	Leu	Pro	Arg	Asn

55

Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu
565 570
Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys
580 585 590
Ala

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1997 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSN06
- (B) CLONE: 828228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCTCCCCGCG	GCGGCTGGCG	TCGGGAAAGT	ACAGTAAAAA	GTCCGAGTGC	AGCCGCCGGG	60
CGCAGGATGG	GATCCGGCTC	CTCCAGCTAC	CGGCCCAAGG	CCATCTACCT	GGACATCGAT	120
GGACGCATTC	AGAAGGTAAT	CTTCAGCAAG	TACTGCAACT	CCAGCGACAT	CATGGACCTG	180
TTCTGCATCG	CCACCGGCCT	GCCTCGGAAC	ACGACCATCT	CCCTGCTGAC	CACCGACGAC	240
GCCATGGTCT	CCATCGACCC	CACCATGCCC	GCGAATTCAG	AACGCACTCC	GTACAAAGTG	300
AGACCTGTGG	CCATCAAGCA	ACTCTCCGCT	GGTGTGAGG	ACAAGAGAAC	CACAAGCCGT	360
GGCCAGTCTG	CTGAGAGACC	ACTGAGGGAC	AGACGGGTG	TGGGCCTGGA	GCAGCCCCGG	420
AGGGAAGGAG	CATTTGAAAG	TGGACAGGTA	GAGCCCAGGC	CCAGAGAGCC	CCAGGGCTGC	480
TACCAGGAAG	GCCAGCGCAT	CCCTCCAGAG	AGAGAAGAAT	TAATCCAGAG	CGTGCTGGCG	540
CAGGTTGCAG	AGCAGTTCTC	AAGAGCATTC	AAAATCAATG	AAGTGAAGC	TGAAGTTGCA	600
AATCACTTGG	CTGTCTTAGA	GAAACGCGTG	GAATTGGAAG	GAATAAAAGT	GGTGGAGATT	660
GAGAAATGCA	AGAGTGACAT	TAAGAAGATG	AGGGAGGAGC	TGGCGGCCAG	AAGCAGCAGG	720
ACCAACTGCC	CCTGTAAGTA	CAGTTTTTTT	GATAACCACA	AGAAAGTGAC	TCCTCGACGC	780
GATGTTCCCA	CTTACCCCAA	GTACCTGCTC	TCTCCAGAGA	CCATCGAGGC	CCTGCGGAAG	840
CCGACCTTTG	ACGTCCTGGC	TTGGGAGCCC	AATGAGATGC	TGAGCTGCCT	GGAGCACATG	900
TACCACGACC	TCGGGCTGGT	CAGGGACTTC	AGCATCAACC	CTGTCAACCT	CAGGAGGTGG	960
CTGTTCTGTG	TCCACGACAA	CTACAGAAAC	AACCCCTTCC	ACAACTTCCG	GCACTGCTTC	1020
TGCGTGGCCC	AGATGATGTA	CAGCATGGTC	TGGCTCTGCA	GTCTCCAGGA	GAAGTTCTCA	1080
CAAACGGATA	TCCTGATCCT	AATGACAGCG	GCCATCTGCC	ACGATCTGGA	CCATCCCCGG	1140
TACAACAACA	CGTACCAGAT	CAATGCCCGC	ACAGAGCTGG	CGGTCCGCTA	CAATGACATC	1200
TCACCGCTGG	AGAACCAACA	CTGCGCCGTG	GCCTTCCAGA	TCCTCGCCGA	GCCTGAGTGC	1260
AACATCTTCT	CCAACATCCC	ACCTGATGGG	TTCAAGCAGA	TCCGACAGGG	AATGATCACA	1320
TTAATCTTGG	CCACTGACAT	GGCAAGACAT	GCAGAAATTA	TGGATTCTTT	CAAAGAGAAA	1380
ATGGAGAATT	TTGACTACAG	CAACGAGGAG	CACATGACCC	TGCTGAAGAT	GATTTTGATA	1440
AAATGCTGTG	ATATCTCTAA	CGAGGTCCGT	CCAATGGAAG	TCGAGAGGCC	TTGGGTGGAC	1500
TGTTTTATTAG	AGGAATATT	TATGAGAGAG	GACCGTGAGA	AGTCAGAAGG	CCTTCCTGTG	1560
GCACCGTTCA	TGGACCGAGA	CAAAGTGACC	AAGGCCACAG	CCCAGATTGG	GTTTCATCAAG	1620
TTTGTCTCTG	TCCCAATGTT	TGAAACAGTG	ACCAAGCTCT	TCCCCATGGT	TGAGGAGATC	1680
ATGCTGCAGC	CACTTTGGGA	ATCCCGAGAT	CGCTACGAGG	AGCTGAAGCG	GATAGATGAC	1740
GCCATGAAAG	AGTTACAGAA	GAAGACTGAC	AGCTTGACGT	CTGGGGCCAC	CGAGAAGTCC	1800
AGAGAGAGAA	GCAGAGATGT	GAAAAACAGT	GAAGGAGACT	GTGCCTGAGG	AAAGCGGGGG	1860
GCGTGGCTGC	AGTTCTGGAC	GGGCTGGCCG	AGCTGCGCGG	GATCCTTGTC	CAGGGAAGAG	1920
CTGCCCTGGG	CACCTGGCAC	CACAAGACCA	TGTTTTCTAA	GAACCATTTT	GTTCACTGAT	1980
ACAAAAA	AAAAA					1997

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1PLB02

(B) CLONE: 156196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu	Ala	Cys	Phe	Leu	Asp	Lys	His	His	Asp	Ile	Ile	Ile	Ile	Asp	His
1				5					10					15	
Arg	Asn	Pro	Arg	Gln	Leu	Asp	Ala	Glu	Ala	Leu	Cys	Arg	Ser	Ile	Arg
			20					25					30		
Ser	Ser	Lys	Leu	Ser	Glu	Asn	Thr	Val	Ile	Val	Gly	Val	Val	Arg	Arg
		35					40					45			
Val	Asp	Arg	Glu	Glu	Leu	Ser	Val	Met	Pro	Phe	Ile	Ser	Ala	Gly	Phe
	50					55					60				
Thr	Arg	Arg	Tyr	Val	Glu	Asn	Pro	Asn	Ile	Met	Ala	Cys	Tyr	Asn	Glu
65					70					75				80	
Leu	Leu	Gln	Leu	Glu	Phe	Gly	Glu	Val	Arg	Ser	Gln	Leu	Lys	Leu	Arg
				85					90					95	
Ala	Cys	Asn	Ser	Val	Phe	Thr	Ala	Leu	Glu	Asn	Ser	Glu	Asp	Ala	Ile
			100					105					110		
Glu	Ile	Thr	Ser	Glu	Asp	Arg	Phe	Ile	Gln	Tyr	Ala	Asn	Pro	Ala	Phe
		115					120					125			
Glu	Thr	Thr	Met	Gly	Tyr	Gln	Ser	Gly	Glu	Leu	Ile	Gly	Lys	Glu	Leu
	130					135					140				
Gly	Glu	Val	Pro	Ile	Asn	Glu	Lys	Lys	Ala	Asp	Leu	Leu	Asp	Thr	Ile
145					150					155					160
Asn	Ser	Cys	Ile	Arg	Ile	Gly	Lys	Glu	Trp	Gln	Gly	Ile	Tyr	Tyr	Ala
				165					170					175	
Lys	Lys	Lys	Asn	Gly	Asp	Asn	Ile	Gln	Gln	Asn	Val	Lys	Ile	Ile	Pro
			180					185					190		
Val	Ile	Gly	Gln	Gly	Gly	Lys	Ile	Arg	His	Tyr	Val	Ser	Ile	Ile	Arg
		195					200					205			
Val	Cys	Asn	Gly	Asn	Asn	Lys	Ala	Glu	Lys	Ile	Ser	Glu	Cys	Val	Gln
	210					215					220				
Ser	Asp	Thr	Arg	Thr	Asp	Asn	Gln	Thr	Gly	Lys	His	Lys	Asp	Arg	Arg
225					230					235					240
Lys	Gly	Ser	Leu	Asp	Val	Lys	Ala	Val	Ala	Ser	Arg	Ala	Thr	Glu	Val
				245					250					255	
Ser	Ser	Gln	Arg	Arg	His	Ser	Ser	Met	Ala	Arg	Ile	His	Ser	Met	Thr
			260					265					270		
Ile	Glu	Ala	Pro	Ile	Thr	Lys	Val	Ile	Asn	Val	Ile	Asn	Ala	Ala	Gln
		275					280					285			
Glu	Ser	Ser	Pro	Met	Pro	Val	Thr	Glu	Ala	Leu	Asp	Arg	Val	Leu	Glu
	290					295					300				
Ile	Leu	Arg	Thr	Thr	Glu	Leu	Tyr	Ser	Pro	Gln	Phe	Gly	Ala	Lys	Asp
305					310					315					320
Asp	Asp	Pro	His	Ala	Asn	Asp	Leu	Val	Gly	Gly	Leu	Met	Ser	Asp	Gly
				325					330					335	
Leu	Arg	Arg	Leu	Ser	Gly	Asn	Glu	Tyr	Val	Leu	Ser	Thr	Lys	Asn	Thr
			340					345					350		
Gln	Met	Val	Ser	Ser	Asn	Ile	Ile	Thr	Pro	Ile	Ser	Leu	Asp	Asp	Val
		355					360					365			
Pro	Pro	Arg	Ile	Ala	Arg	Ala	Met	Glu	Asn	Glu	Glu	Tyr	Trp	Asp	Phe
	370					375						380			
Asp	Ile	Phe	Glu	Leu	Glu	Ala	Ala	Thr	His	Asn	Arg	Pro	Leu	Ile	Tyr
385					390					395					400
Leu	Gly	Leu	Lys	Met	Phe	Ala	Arg	Phe	Gly	Ile	Cys	Glu	Phe	Leu	His
				405					410					415	
Cys	Ser	Glu	Ser	Thr	Leu	Arg	Ser	Trp	Leu	Gln	Ile	Ile	Glu	Ala	Asn
			420					425					430		
Tyr	His	Ser	Ser	Asn	Pro	Tyr	His	Asn	Ser	Thr	His	Ser	Ala	Asp	Val
		435					440					445			
Leu	His	Ala	Thr	Ala	Tyr	Phe	Leu	Ser	Lys	Glu	Arg	Ile	Lys	Glu	Thr
	450					455					460				
Leu	Asp	Pro	Ile	Asp	Glu	Val	Ala	Ala	Leu	Ile	Ala	Ala	Thr	Ile	His
465					470					475					480
Asp	Val	Asp	His	Pro	Gly	Arg	Thr	Asn	Ser	Phe	Leu	Cys	Asn	Ala	Gly
				485					490					495	

Ser Glu Leu Ala Ile Leu Tyr Asn Asp Thr Ala Val Leu Glu Ser His
500 505 510
His Ala Ala Leu Ala Phe Gln Leu Thr Thr Gly Asp Asp Lys Cys Asn
515 520 525
Ile Phe Lys Asn Met Glu Arg Asn Asp Tyr Arg Thr Leu Arg Gln Gly
530 535 540
Ile Ile Asp Met Val Leu Ala Thr Glu Met Thr Lys His Phe Glu His
545 550 555 560
Val Asn Lys Phe Val Asn Ser Ile Asn Lys Pro Leu Ala Thr Leu Glu
565 570 575
Glu Asn Gly Glu Thr Asp Lys Asn Gln Glu Val Ile Asn Thr Met Leu
580 585 590
Arg Thr Pro Glu Asn Arg Thr Leu Ile Lys Arg Met Leu Ile Lys Cys
595 600 605
Ala Asp Val Ser Asn Pro Cys Arg Pro Leu Gln Tyr Cys Ile Glu Trp
610 615 620
Ala Ala Arg Ile Ser Glu Glu Tyr Phe Ser Gln Thr Asp Glu Glu Lys
625 630 635 640
Gln Gln Gly Leu Pro Val Val Met Pro Val Phe Asp Arg Asn Thr Cys
645 650 655
Ser Ile Pro Lys Ser Gln Ile Ser Phe Ile Asp Tyr Phe Ile Thr Asp
660 665 670
Met Phe Asp Ala Trp Asp Ala Phe Val Asp Leu Pro Asp Leu Met Gln
675 680 685
His Leu Asp Asn Asn Phe Lys Tyr Trp Lys Gly Leu Asp Glu Met Lys
690 695 700
Leu Arg Asn Leu Arg Pro Pro Pro Glu
705 710

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 829179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Phe Gln His Gln Thr Asn Pro Gly Gly Pro Thr Asn Arg Arg Arg
1 5 10 15
Pro Arg Asp Gln Glu Ile His Gln Glu Pro Arg Tyr Pro Lys Ala Arg
20 25 30
Arg His Thr Pro Ala Trp Pro Pro Thr Gln Ser Arg Ser Trp Thr Gly
35 40 45
Ala Ser Thr Ser Trp Arg Pro Ser Arg Pro Ile Ala Ala Ser Pro Thr
50 55 60
Trp Arg Arg Leu Ser Ser Asn Ala Cys Ser Thr Arg Ser Cys Arg Thr
65 70 75 80
Leu Ala Ser Pro Ala Asp Arg Glu Ile Arg Phe Pro Asn Ile Tyr Val
85 90 95
Pro His Phe Trp Asp Lys Gln Gln Glu Phe Asp Leu Pro Ser Leu Arg
100 105 110
Val Glu Asp Asn Pro Glu Leu Val Ala Ala Asn Ala Ala Gly Gln
115 120 125
Gln Ser Ala Gly Gln Tyr Ala Arg Ser Arg Ser Pro Arg Gly Pro Pro
130 135 140
Met Ser Gln Ile Ser Gly Val Lys Arg Pro Leu Ser His Thr Asn Ser
145 150 155 160
Phe Thr Gly Glu Arg Leu Pro Thr Phe Gly Val Glu Thr Pro Arg Glu
165 170 175
Asn Glu Leu Gly Thr Leu Leu Gly Glu Leu Asp Thr Trp Gly Ile Gln

180 185 190
 Ile Phe Ser Ile Gly Glu Phe Ser Val Asn Arg Pro Leu Thr Cys Val
 195 200 205
 Ala Tyr Thr Ile Phe Gln Ser Arg Glu Leu Leu Thr Ser Leu Met Ile
 210 215 220
 Pro Pro Lys Thr Phe Leu Asn Phe Met Ser Thr Leu Glu Asp His Tyr
 225 230 235 240
 Val Lys Asp Asn Pro Phe His Asn Ser Leu His Ala Ala Asp Val Thr
 245 250 255
 Gln Ser Thr Asn Val Leu Leu Asn Thr Pro Ala Leu Glu Gly Val Phe
 260 265 270
 Thr Pro Leu Glu Val Gly Gly Ala Leu Phe Ala Ala Cys Ile His Asp
 275 280 285
 Val Asp His Pro Gly Leu Thr Asn Gln Phe Leu Val Asn Ser Ser Ser
 290 295 300
 Glu Leu Ala Leu Met Tyr Asn Asp Glu Ser Val Leu Glu Asn His His
 305 310 315 320
 Leu Ala Val Ala Phe Lys Leu Leu Gln Asn Gln Gly Cys Asp Ile Phe
 325 330 335
 Cys Asn Met Gln Lys Lys Gln Arg Gln Thr Leu Arg Lys Met Val Ile
 340 345 350
 Asp Ile Val Leu Ser Thr Asp Met Ser Lys His Met Ser Leu Leu Ala
 355 360 365
 Asp Leu Lys Thr Met Val Glu Thr Lys Lys Val Ala Gly Ser Gly Val
 370 375 380
 Leu Leu Leu Asp Asn Tyr Thr Asp Arg Ile Gln Val Leu Glu Asn Leu
 385 390 395 400
 Val His Cys Ala Asp Leu Ser Asn Pro Thr Lys Pro Leu Pro Leu Tyr
 405 410 415
 Lys Arg Trp Val Ala Leu Leu Met Glu Glu Phe Phe Leu Gln Gly Asp
 420 425 430
 Lys Glu Arg Glu Ser Gly Met Asp Ile Ser Pro Met Cys Asp Arg His
 435 440 445
 Asn Ala Thr Ile Glu Lys Ser Gln Val Gly Phe Ile Asp Tyr Ile Val
 450 455 460
 His Pro Leu Trp Glu Thr Trp Ala Ser Leu Val His Pro Asp Ala Gln
 465 470 475 480
 Asp Ile Leu Asp Thr Leu Glu Glu Asn Arg Asp Tyr Tyr Gln Ser Met
 485 490 495
 Ile Pro Pro Ser Pro Pro Pro Ser Gly Val Asp Glu Asn Pro Gln Glu
 500 505 510
 Asp Arg Ile Arg Phe Gln Val Thr Leu Glu Glu Ser Asp Gln Glu Asn
 515 520 525
 Leu Ala Glu Leu Glu Glu Gly Asp Glu Ser Gly Gly Glu Thr Thr Thr
 530 535 540
 Thr Gly Thr Thr Gly Thr Ala Ala Ser Ala Leu Arg Ala Gly Gly
 545 550 555 560
 Gly Gly Gly Gly Gly Gly Gly Met Ala Pro Arg Thr Gly Gly Cys Gln
 565 570 575
 Asn Gln Pro Gln His Gly Gly Met
 580

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGGTGACAGG GTTGATGCT

19

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCGCTTAGTT TTACCGTTTT C

21

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TATCGCCTCC ATCAACAAAC TT

22

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GACACAGAAC AGCCACCTC

19

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGCAAGTTCA GCCTGGTTAA G

21

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTTATGAGTA TTTCTTCCAG GGTA

24

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCATGGTTA CAAATTATCG AAGCCAATTA

30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCTCCTCCCT CATCTTCTTA

20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGGACAGCCA AGTGATTT

18

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCGCTGGCC TTCCTGGTAG

20